

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Friedman, Jeffrey M.
Lee, Gwo-Hua
Proenca, Ricardo

(ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC ACIDS ENCODING THE RECEPTOR, AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 54

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David A. Jackson, Esq.
(B) STREET: 411 Hackensack Ave, Continental Plaza, 4th Floor
(C) CITY: Hackensack
(D) STATE: New Jersey
(E) COUNTRY: USA
(F) ZIP: 07601

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Jackson Esq., David A.
(B) REGISTRATION NUMBER: 66,742
(C) REFERENCE/DOCKET NUMBER: 600-1-162

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 201-487-5800
(B) TELEFAX: 201-343-1684

(x) Note: In all the amino acid sequences below, "Xaa" stands for one of the three stop codons.

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A15 (OB-Ra)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA GGCCTCTCG	60
CCATGCCGGA TCAGCACCAAG CTTGTAGCTC GTGCCGAATT CGGCACGGAGG TTGCTTGGG	120
AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA GACACTGGCT	180
TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT AGAGTGCTGG	240
ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA GAACCCCTTC	300
AAGAATTATG ACTCTAACGGT CCATTTTA TATGATCTGC CTGAAGTCAT AGATGATTG	360
CCTCTGCCCG CACTGAAAGA CAGCTTCAG ACTGTCCAAT GCAACTGCAG TCTTCGGGG	420
TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTCT GATGTATTTG	480
GAAATCACAT CTGCCGGTGT GAGTTTCAG TCACCTCTGA TGTCACTGCA GCCCATGCTT	540
GTTGTGAAAC CCGATCCACC CTTAGGTTG CATATGGAAG TCACAGATGA TGGTAATTAA	600
AAGATTTCTT GGGACAGCCA AACAAATGGCA CCATTTCCGC TTCAATATCA GGTGAAATAT	660
TTAGAGAATT CTACAATTGT AAGAGAGGCT GCTGAAATTG TCTCAGCTAC ATCTCTGCTG	720
GTAGACAGTG TGCTTCCTGG ATCTTCATAT GAGGTCCAGG TGAGGAGCAA GAGACTGGAT	780
GGTCAGGAG TCTGGAGTGA CTGGAGTTCA CCTCAAGTCT TTACCACACA AGATGTTGTG	840
TATTTTCCAC CAAAATTCT GACTAGTGT GGATCGAATG CTTCTTTCA TTGCATCTAC	900
AAAAACGAAA ACCAGATTAT CTCCTAAAA CAGATAGTTT GGTGGAGGAA TCTAGCTGAG	960
AAAATCCCTG AGATACAGTA CAGCATTGTG AGTGACCGAG TTAGCAAAGT TACCTCTCC	1020
AACCTGAAAG CCACCAGACC TCGAGGGAAAG TTTACCTATG ACGCAGTGT A CTGCTGCAAT	1080
GAGCAGGCCT GCCATCACCG CTATGCTGAA TTATACGTGA TCGATGTCAA TATCAATATA	1140
TCATGTGAAA CTGACGGGTAA CTTAACTAAA ATGACTTGCA GATGGTCACC CAGCACAATC	1200
CAATCACTAG TGGGAAGCAC TGTGCAGCTG AGGTATCACA GGCGCAGCCT GTATTGTCCT	1260
GATAGTCCAT CTATTCTAC TACGTCTGAG CCCAAAAACT GCGTCTTACA GAGAGACGGC	1320
TTTTATGAAT GTGTTTCCA GCCAATCTT CTATTATCTG GCTATACAAT GTGGATCAGG	1380
ATCAACCATT CTTTAGGTTC ACTTGACTCG CCACCAACGT GTGTCTTCC TGACTCCGTA	1440
GTAAAACCAC TACCTCCATC TAACGTAAAA GCAGAGATTA CTGTAAACAC TGGATTATTG	1500
AAAGTATCTT GGGAAAAGCC AGTCTTCCG GAGAATAACC TTCAATTCCA GATTGATAT	1560
GGCTTAAGTG GAAAAGAAAT ACAATGGAAG ACACATGAGG TATTCGATGC AAAGTCAAAG	1620
TCTGCCAGCC TGCTGGTGTC AGACCTCTGT GCAGTCTATG TGGTCCAGGT TCGCTGCCGG	1680
CGGTTGGATG GACTAGGATA TTGGAGTAAT TGGAGCAGTC CAGCCTATAC GCTTGTCTG	1740
GATGTAAAAG TTCCTATGAG AGGGCCTGAA TTTTGGAGAA AAATGGATGG GGACGTTACT	1800
AAAAAGGAGA GAAATGTCAC CTTGCTTGG AAGCCCTGA CGAAAAATGA CTCACTGTGT	1860
AGTGTGAGGA GGTACGTGGT GAAGCATCGT ACTGCCACCA ATGGGACGTG GTCAGAAGAT	1920

GTGGGAAATC GGACCAATCT CACTTCCTG TGGACAGAAC CAGCGCACAC TGTTACAGTT	1980
CTGGCTGTCA ATTCCCTCGG CGCTTCCCTT GTGAATTAA ACCTTACCTT CTCATGGCCC	2040
ATGAGTAAAG TGAGTGTGT GGAGTCACTC AGTGCTTATC CCCTGAGCAG CAGCTGTGTC	2100
ATCCTTCCTT GGACACTGTC ACCTGATGAT TATAGTCTGT TATATCTGGT TATTGAATGG	2160
AAGATCCTTA ATGAAGATGA TGGAAATGAAG TGGCTTAGAA TTCCCTCGAA TGTTAAAAAG	2220
TTTTATATCC ACGATAATT TATTCCCATC GAGAAATATC AGTTTAGTCT TTACCCAGTA	2280
TTTATGGAAG GAGTTGGAAA ACCAAAGATA ATTAATGGTT TCACCAAAGA TGCTATCGAC	2340
AAGCAGCAGA ATGACGCAGG GCTGTATGTC ATTGTACCCA TAATTATTC CTCTTGTGTC	2400
CTACTGCTCG GAACACTGTT AATTCACAC CAGAGAATGA AAAAGTTGTT TTGGGACGAT	2460
GTTCCAAACC CCAAGAATTG TTCCTGGCA CAAGGACTGA ATTTCCAAAA GAGAACGGAC	2520
ACTCTTTGA	2529

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 842 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly	Leu	Arg	Ser	Ala	Ser	Tyr	Gln	Pro	Leu	Lys	Arg	Phe	Ser	Arg	Phe
1					5					10				15	
Gln	Ala	Leu	Ser	Pro	Cys	Arg	Ile	Ser	Thr	Ser	Leu	Xaa	Leu	Val	Pro
		20						25					30		
Asn	Ser	Ala	Arg	Gly	Cys	Phe	Gly	Asn	Glu	Gln	Gly	Gln	Asn	Cys	Ser
				35				40				45			
Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala	Ser	Val	Val	Lys
		50				55					60				
Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp	Ile	Glu	Cys	Trp
		65			70				75				80		
Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met	Glu	Pro	Leu	Pro
				85			90				95				
Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His	Leu	Leu	Tyr	Asp
				100				105				110			

Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro Leu Lys Asp Ser
 115 120 125
 Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly Cys Glu Cys His
 130 135 140
 Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu Leu Met Tyr Leu
 145 150 155 160
 Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro Leu Met Ser Leu
 165 170 175
 Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu Gly Leu His Met
 180 185 190
 Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp Asp Ser Gln Thr
 195 200 205
 Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr Leu Glu Asn Ser
 210 215 220
 Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala Thr Ser Leu Leu
 225 230 235 240
 Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val Gln Val Arg Ser
 245 250 255
 Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp Ser Ser Pro Gln
 260 265 270
 Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro Lys Ile Leu Thr
 275 280 285
 Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr Lys Asn Glu Asn
 290 295 300
 Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg Asn Leu Ala Glu
 305 310 315 320
 Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp Arg Val Ser Lys
 325 330 335
 Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg Gly Lys Phe Thr
 340 345 350
 Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys His His Arg Tyr
 355 360 365
 Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile Ser Cys Glu Thr
 370 375 380
 Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser Pro Ser Thr Ile
 385 390 395 400
 Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr His Arg Arg Ser
 405 410 415
 Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr Ser Glu Pro Lys
 420 425 430
 Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys Val Phe Gln Pro
 435 440 445
 Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser
 450 455 460

Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val
 465 470 475 480

Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu Ile Thr Val Asn
 485 490 495

Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val Phe Pro Glu Asn
 500 505 510

Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Ile Gln
 515 520 525

Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys Ser Ala Ser Leu
 530 535 540

Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln Val Arg Cys Arg
 545 550 555 560

Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser Ser Pro Ala Tyr
 565 570 575

Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly Pro Glu Phe Trp
 580 585 590

Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg Asn Val Thr Leu
 595 600 605

Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys Ser Val Arg Arg
 610 615 620

Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr Trp Ser Glu Asp
 625 630 635 640

Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr Glu Pro Ala His
 645 650 655

Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala Ser Leu Val Asn
 660 665 670

Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val Ser Ala Val Glu
 675 680 685

Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val Ile Leu Ser Trp
 690 695 700

Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu Val Ile Glu Trp
 705 710 715 720

Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu Arg Ile Pro Ser
 725 730 735

Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile Pro Ile Glu Lys
 740 745 750

Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly Val Gly Lys Pro
 755 760 765

Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp Lys Gln Gln Asn
 770 775 780

Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile Ser Ser Cys Val
 785 790 795 800

Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
 805 810 815

Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
 820 825 830

Leu Asn Phe Gln Lys Arg Thr Asp Thr Leu
 835 840

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2848 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: A40 (OB-Rb)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCATTGAGA	GTGCCAACGG	GAAGGCTTAA	TTAACCTTG	GAANTGAGTC	CGAAGAGTCT	60
GGAAGTNTGT	AAGATGGAAG	ATACTATACA	AGATACTTCA	GAGCTGTACA	TTCTTCCAGG	120
GATGTAGGCT	AGCAGTTATT	TCATTAGTAT	ATGTCTATT	TAGAATGGGA	AGAATTAGGA	180
AGATGAATGG	AGCCTGTGTC	TTTCACTACT	CTCCCAGGAG	GTTCCAGAAT	AGCNAAAGTG	240
TCAGCCAGAA	TTCTTGAAGT	CATAGACTGG	AGTTAGAGAT	GAACATAAGC	TCATGTTAAG	300
CCTGGGTTAC	TTCTTATCAT	CCTTAATT	GAAAGCTAAC	AGGGCCTAAC	CATCAAGAAC	360
GTCCTGGAGG	AAAGAATGTT	TTAACGCCA	TTATTCAGTC	AAAGAAATTA	AGACTTGAGA	420
GAAATGCTCA	TTTCTTCTCT	CATGATGGCT	CCTTACACCT	TACTTCTACC	GTACGATCCA	480
TGNGGCCTA	CCCACCGCAGG	ATACATGCAT	CTATATGAGA	GTGTCTNCCC	CTTCTAACTC	540
AGAGACTCTT	GTTCTAGTCT	GTGNTATAAA	ATTCAGCTTG	TGGAAGCTTT	CTGAGGGGTT	600
GGCAGCATTC	AATTTTACCT	GCAATAGGTA	AAGGTAATCT	TTTGGGAAGT	GAAGAGTGTT	660
ATTAGACATT	TCAGAAAGAA	CAAACAGGAT	TGGGGCTGCT	ATGTGTTCTA	CACAGGAATC	720
TTCCATAACA	CAGAATAATT	TATGTAGATA	GAGACAAGAT	GGAAATGCC	AGGGCCCCAA	780
AATAGCCGCT	GTTATTGTT	AACCTTCAAG	GTTTCTGTT	TGTTTATCTG	TTCTTGC	840
AGGATCATCT	TCCAAGCACA	TCCTGGGGGA	ACAGTGGCAG	AGTCACTCGA	GTTCATGAAA	900
CTATGGTGAC	ATCTGAGCTT	CCTTGGTTCT	TCACAGAAC	TAAGCAGTTC	CTTGTCTGC	960
TTGTTAGATG	AGAAAACCTTC	CTTGTCAAGTC	TGTCTCTACG	ACTAGAATGG	AAAGCCTTAC	1020
TACTTCCTAT	GTATTCTTAA	TATTCAAAT	GTCTAAATTA	TGTTTGGCTT	CTCTGTCTTT	1080
AAGGGATTAA	GTCTCTGGAT	TTGAAGAAAT	AAATAAATAA	ATAAAGGAAA	ACTAATTTC	1140

TCGTGCCGGA	TGACTGCTAG	CTGAGCTCAG	GCCTACTGCA	TTCTACATTT	CGACTCTCTC	1200
CCTCTTCCCC	AGTGCTTAG	CACTGGACTG	GGCAGTNCCCT	GGCCTGGTCT	AACTCCTGTT	1260
TCCTGGTGGG	AATGTATAAT	AAGAACTCCA	TGAGTTCTGG	TATAAACACT	GTGGTCTGTG	1320
TGCTAATTAA	ATCTNGTGT	TCCTACAGCC	CCTGACGAAA	AATGACTCAC	TGTGTAGTGT	1380
GAGGAGGTAC	GTGGTGAAGC	ATCGTACTGC	CCACAATGGG	ACGTGGTCAG	AAGATGTGGG	1440
AAATCGGACC	AATCTCACTT	TCCTGTGGAC	AGAACCCAGCG	CACACTGTTA	CAGTTCTGGC	1500
TGTCAATTCC	CTCGGCGCTT	CCCTTGTGAA	TTTTAACCTT	ACCTTCTCAT	GGCCCATGAG	1560
TAAAGTGAGT	GCTGTGGAGT	CACTCAGTGC	TTATCCCCTG	AGCAGCAGCT	GTGTCATCCT	1620
TTCCCTGGACA	CTGTCACCTG	ATGATTATAG	TCTGTTATAT	CTGGTTATTG	AATGGAAGAT	1680
CCTTAATGAA	GATGATGGAA	TGAAGTGGCT	TAGAATTCCC	TCGAATGTTA	AAAAGTTTA	1740
TATCCACGAT	AATTTTATTC	CCATCGAGAA	ATATCAGTTT	AGTCTTACCC	CAGTATTTAT	1800
GGAAGGAGTT	GGAAAACCAA	AGATAATTAA	TGGTTTCACC	AAAGATGCTA	TCGACAAAGCA	1860
GCAGAATGAC	GCAGGGCTGT	ATGTCATTGT	ACCCATAATT	ATTTCCCTTT	GTGTCCTACT	1920
GCTCGGAACA	CTGTTAATTT	CACACCAGAG	AATGAAAAAG	TTGTTTGAGG	ACGATGTTCC	1980
AAACCCCAAG	AATTGTTCCCT	GGGCACAAGG	ACTGAATTTC	CAAAAGCCTG	AAACATTNGA	2040
GCATCTTTT	ACCAAGCATG	CAGAACATCGT	GATATTGGT	CCTCTCTTC	TGGAGCCTGA	2100
ACCCATTCA	GAAGAAATCA	GTGTCGATAC	AGCTTGGAAA	AATAAAGATG	AGATGGTCCC	2160
AGCAGCTATG	GTCTCCCTNC	TNNGGACAC	ACCAGACCCCT	GAAAGCAGTT	CTATTTGTNT	2220
TAGTGACCAG	TGTAACAGTG	CTAACTTCTC	TGGGTCTCAG	AGCACCCAGG	TAACCTGTGA	2280
GGATGAGTGT	CAGAGACAAC	CCTCAGTTAA	ATATGCAACT	CTGGTCAGCA	ACGATAAAACT	2340
AGTGGAAACT	GATGAAGAGC	AAGGGTTTAT	CCATAGTCCT	GTCAGCAACT	GCATCTCCAG	2400
TAATCATTCC	CCACTGAGGC	AGTCTTCTC	TAGCAGCTCC	TGGGAGACAG	AGGCCAGAC	2460
ATTTTCCTT	TTATCAGACC	AGCAACCCAC	CATGATTCA	CCACAACTTT	CATTCTCGGG	2520
GTTGGATGAG	CTTTTGGAAC	TGGAGGGAAAG	TTTCCTGAA	GAAAATCACA	GGGAGNAGTC	2580
TGTCTGTTAT	CTAGGAGTCA	CCTCCGTCCN	CAGAAGAGAG	AGTGGTGTGC	TTTGACTGG	2640
TGAGGCAGGA	ATCCTGTGCA	CATTCCCAGC	CCAGTGCTG	TTCAAGTGACA	TCAGGATCCT	2700
CCAGGAGAGA	TGCTCACACT	TTGTAGAAAA	TAATTTGAGT	TTAGGGACCT	CTGGTGAGAA	2760
CTTTGGTCCT	AACATGCC	AATTCCAAAC	CTGTTCCACG	CACAGTCACA	AGATAATGGA	2820
GAATAAGATG	TGTGACTTAA	CTGTGTAA				2848

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 581 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu	Arg	Asp	Leu	Val	Ser	Gly	Phe	Glu	Glu	Ile	Asn	Lys	Ile	Lys	Glu
1					5				10						15
Asn	Phe	Ser	Arg	Ala	Gly	Leu	Leu	Ala	Glu	Leu	Arg	Pro	Thr	Ala	Phe
	20							25						30	
Tyr	Ile	Ser	Thr	Leu	Ser	Leu	Phe	Pro	Ser	Ala	Leu	Ala	Leu	Asp	Trp
	35					40							45		
Ala	Val	Pro	Gly	Leu	Val	Leu	Leu	Phe	Pro	Gly	Gly	Asn	Val	Glu	Leu
	50					55					60				
His	Glu	Phe	Trp	Tyr	Lys	His	Cys	Gly	Leu	Cys	Ala	Asn	Ile	Xaa	Cys
	65				70				75					80	
Phe	Leu	Gln	Pro	Leu	Thr	Lys	Asn	Asp	Ser	Leu	Cys	Ser	Val	Arg	Arg
		85						90						95	
Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His	Asn	Gly	Thr	Trp	Ser	Glu	Asp
	100						105						110		
Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe	Leu	Trp	Thr	Glu	Pro	Ala	His
	115						120					125			
Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser	Leu	Gly	Ala	Ser	Leu	Val	Asn
	130					135						140			
Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met	Ser	Lys	Val	Ser	Ala	Val	Glu
	145				150					155				160	
Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser	Ser	Cys	Val	Ile	Leu	Ser	Trp
		165						170					175		
Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu	Leu	Tyr	Leu	Val	Ile	Glu	Trp
	180					185						190			
Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met	Lys	Trp	Leu	Arg	Ile	Pro	Ser
		195					200					205			
Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp	Asn	Phe	Ile	Pro	Ile	Glu	Lys
		210				215						220			
Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe	Met	Glu	Gly	Val	Gly	Lys	Pro
	225					230				235				240	
Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp	Ala	Ile	Asp	Lys	Gln	Gln	Asn
			245					250					255		
Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro	Ile	Ile	Ile	Ser	Ser	Cys	Val
		260					265					270			

Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg Met Lys Lys Leu
 275 280 285
 Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser Trp Ala Gln Gly
 290 295 300
 Leu Asn Phe Gln Lys Pro Glu Thr Phe Glu Gln Leu Phe Thr Lys His
 305 310 315 320
 Ala Glu Ser Val Ile Phe Gly Pro Leu Leu Leu Glu Pro Glu Pro Ile
 325 330 335
 Ser Glu Glu Ile Ser Val Asp Thr Ala Trp Lys Asn Lys Asp Glu Met
 340 345 350
 Val Pro Ala Ala Met Val Ser Leu Leu Trp Thr Thr Pro Asp Pro Glu
 355 360 365
 Ser Ser Ser Ile Cys Ile Ser Asp Gln Cys Asn Ser Ala Asn Phe Ser
 370 375 380
 Gly Ser Gln Ser Thr Gln Val Cys Glu Asp Glu Cys Gln Arg Gln Pro
 385 390 395 400
 Ser Val Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr
 405 410 415
 Asp Glu Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser
 420 425 430
 Ser Asn His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Trp Glu
 435 440 445
 Thr Glu Ala Gln Thr Phe Phe Leu Leu Ser Asp Gln Gln Pro Thr Met
 450 455 460
 Ile Ser Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu
 465 470 475 480
 Glu Gly Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr
 485 490 495
 Leu Gly Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr
 500 505 510
 Gly Glu Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser
 515 520 525
 Asp Ile Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn
 530 535 540
 Leu Ser Leu Gly Thr Ser Gly Glu Asn Phe Gly Pro Tyr Met Pro Gln
 545 550 555 560
 Phe Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met
 565 570 575
 Cys Asp Phe Thr Val
 580

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 961 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: A6 (OB-Rc)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTAAGGGAT TTAGTCTCTG GATTTGAAGA AATAAATAAA TAAATAAAGG AAAACTAATT	60
TTCTCGTGCC GGATGACTGC TAGCTGAGCT CAGGCCTACT GCATTCTACA TTTCGACTCT	120
CTCCCTCTTC CCCAGTGCTT TAGCACTGGA CTGGGCAGTN CCTGGCCTGG TCTAACCTCCT	180
GTTTCTGGT GGGAAATGTAT AATAAGAACT CCATGAGTTC TGGTATAAAC ACTGTGGTCT	240
GTGTGCTAAT TAAATCTNGT GTTTCCTACA GCCCCTGACG AAAAATGACT CACTGTGTAG	300
TGTGAGGAGG TACGTGGTGA AGCATCGTAC TGCCCACAAT GGGACGTGGT CAGAAGATGT	360
GGGAAATCGG ACCAATCTCA CTTTCCTGTG GACAGAACCA GCGCACACTG TTACAGTTCT	420
GGCTGTCAAT TCCCTCGGCG CTTCCCTTGT GAATTTAAC CTTACCTTCT CATGGCCCAT	480
GAGTAAAGTG AGTGCTGTGG AGTCACTCAG TGCTTATCCC CTGAGCAGCA GCTGTGTCA	540
CCTTCCTGG ACACGTGTCAC CTGATGATTA TAGTCTGTTA TATCTGTTA TTGAATGGAA	600
GATCCTTAAT GAAGATGATG GAATGAAGTG GCTTAGAATT CCCTCGAATG TTAAAAAGTT	660
TTATATCCAC GATAATTTA TTCCCATCGA GAAATATCAG TTTAGTCTTT ACCCAGTATT	720
TATGGAAGGA GTTGGAAAAC CAAAGATAAT TAATGGTTTC ACCAAAGATG CTATCGACAA	780
GCAGCAGAAT GACGCAGGGC TGTATGTCAT TGTACCCATA ATTATTTCCT CTTGTGTCC	840
ACTGCTCGGA ACACGTGTTAA TTTCACACCA GAGAATGAAA AAGTTGTTT GGGACGATGT	900
TCCAAACCCC AAGAATTGTT CCTGGGCACA AGGACTGAAT TTCCAAAAGG TCACTGTTA	960
A	961

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu	Arg	Asp	Leu	Val	Ser	Gly	Phe	Glu	Glu	Ile	Asn	Lys	Xaa	Ile	Lys
1					5				10						15
Glu	Asn	Xaa	Phe	Ser	Arg	Ala	Gly	Xaa	Leu	Leu	Ala	Glu	Leu	Arg	Pro
					20				25					30	
Thr	Ala	Phe	Tyr	Ile	Ser	Thr	Leu	Ser	Leu	Phe	Pro	Ser	Ala	Leu	Ala
				35				40					45		
Leu	Asp	Trp	Ala	Val	Pro	Gly	Leu	Val	Xaa	Leu	Leu	Phe	Pro	Gly	Gly
				50				55					60		
Asn	Val	Xaa	Xaa	Glu	Leu	His	Glu	Phe	Trp	Tyr	Lys	His	Cys	Gly	Leu
				65			70			75				80	
Cys	Ala	Asn	Xaa	Ile	Xaa	Cys	Phe	Leu	Gln	Pro	Leu	Thr	Lys	Asn	Asp
				85				90					95		
Ser	Leu	Cys	Ser	Val	Arg	Arg	Tyr	Val	Val	Lys	His	Arg	Thr	Ala	His
				100				105					110		
Asn	Gly	Thr	Trp	Ser	Glu	Asp	Val	Gly	Asn	Arg	Thr	Asn	Leu	Thr	Phe
				115			120					125			
Leu	Trp	Thr	Glu	Pro	Ala	His	Thr	Val	Thr	Val	Leu	Ala	Val	Asn	Ser
				130			135				140				
Leu	Gly	Ala	Ser	Leu	Val	Asn	Phe	Asn	Leu	Thr	Phe	Ser	Trp	Pro	Met
				145			150			155				160	
Ser	Lys	Val	Ser	Ala	Val	Glu	Ser	Leu	Ser	Ala	Tyr	Pro	Leu	Ser	Ser
				165				170					175		
Ser	Cys	Val	Ile	Leu	Ser	Trp	Thr	Leu	Ser	Pro	Asp	Asp	Tyr	Ser	Leu
				180			185					190			
Leu	Tyr	Leu	Val	Ile	Glu	Trp	Lys	Ile	Leu	Asn	Glu	Asp	Asp	Gly	Met
				195				200				205			
Lys	Trp	Leu	Arg	Ile	Pro	Ser	Asn	Val	Lys	Lys	Phe	Tyr	Ile	His	Asp
				210			215				220				
Asn	Phe	Ile	Pro	Ile	Glu	Lys	Tyr	Gln	Phe	Ser	Leu	Tyr	Pro	Val	Phe
				225			230			235			240		
Met	Glu	Gly	Val	Gly	Lys	Pro	Lys	Ile	Ile	Asn	Gly	Phe	Thr	Lys	Asp
				245				250				255			
Ala	Ile	Asp	Lys	Gln	Gln	Asn	Asp	Ala	Gly	Leu	Tyr	Val	Ile	Val	Pro
				260				265				270			
Ile	Ile	Ile	Ser	Ser	Cys	Val	Leu	Leu	Leu	Gly	Thr	Leu	Leu	Ile	Ser
				275				280				285			
His	Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys
				290			295				300				
Asn	Cys	Ser	Trp	Ala	Gln	Gly	Leu	Asn	Phe	Gln	Lys	Val	Thr	Val	

305

310

315

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2703 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: A8 (OB-Rd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGATGTGTC AGAAATTCTA TGTGGTTTG TTACACTGGG AATTTCTTTA TGTGATAGCT	60
GCACCTAACCC TGGCATATCC AATCTCTCCC TGGAAATTAA AGTTGTTTG TGGACCACCG	120
AACACAAACCG ATGACTCCTT TCTCTCACCT GCTGGAGCCC CAAACAATGC CTCGGCTTG	180
AAGGGGGCTT CTGAAGCAAT TGTTGAAGCT AAATTTAATT CAAGTGGTAT CTACGTTCT	240
GAGTTATCCA AACACAGTCTT CCACGTGTC TTTGGGAATG AGCAAGGTCA AAACTGCTCT	300
GCACTCACAG ACAACACTGA AGGGAAGACA CTGGCTTCAG TAGTGAAGGC TTCAGTTTT	360
CGCCAGCTAG GTGTAAACTG GGACATAGAG TGCTGGATGA AAGGGGACTT GACATTATT	420
ATCTGTCATA TGGAGCCATT ACCTAAGAAC CCCTTCAAGA ATTATGACTC TAAGGTCCAT	480
CTTTTATATG ATCTGCCTGA AGTCATAGAT GATTGCCTC TGCCCCACT GAAAGACAGC	540
TTTCAGACTG TCCAATGCAA CTGCAGTCTT CGGGGATGTG AATGTCATGT GCCGGTACCC	600
AGAGCCAAAC TCAACTACGC TCTTCTGATG TATTTGGAAA TCACATCTGC CGGTGTGAGT	660
TTTCAGTCAC CTCTGATGTC ACTGCAGCCC ATGCTTGTG TGAAACCCGA TCCACCCCTTA	720
GGTTTGCATA TGGAAGTCAC AGATGATGGT AATTTAAAGA TTTCTGGGA CAGCCAAACAA	780
ATGGCACCATT TTCCGCTTCA ATATCAGGTG AAATATTTAG AGAATTCTAC AATTGTAAGA	840
GAGGCTGCTG AAATTGTCTC AGCTACATCT CTGCTGGTAG ACAGTGTGCT TCCTGGATCT	900
TCATATGAGG TCCAGGTGAG GAGCAAGAGA CTGGATGGTT CAGGAGTCTG GAGTGACTGG	960
AGTTCACCTC AAGTCTTAC CACACAAGAT GTTGTGTATT TTCCACCCAA AATTCTGACT	1020
AGTGTGGAT CGAATGCTTC TTTTCATTGC ATCTACAAAA ACGAAAACCA GATTATCTCC	1080
TCAAAACAGA TAGTTGGTG GAGGAATCTA GCTGAGAAAA TCCCTGAGAT ACAGTACAGC	1140
ATTGTGAGTG ACCGAGTTAG CAAAGTTACC TTCTCCAACC TGAAAGCCAC CAGACCTCGA	1200
GGGAAGTTA CCTATGACGC AGTGTACTGC TGCAATGAGC AGGCGTGCCA TCACCGCTAT	1260

GCTGAATTAT	ACGTGATCGA	TGTCAATATC	AATATATCAT	GTGAAACTGA	CGGGTACTTA	1320
ACTAAAATGA	CTTGCAGATG	GTCACCCAGC	ACAATCCAAT	CACTAGTGGG	AAGCACTGTG	1380
CAGCTGAGGT	ATCACAGGCG	CAGCCTGTAT	TGTCCTGATA	GTCCCATCTAT	TCATCCTACG	1440
TCTGAGGCCA	AAAAC TGC GT	CTTACAGAGA	GACGGCTTTT	ATGAATGTGT	TTTCCAGCCA	1500
ATCTTCTAT	TATCTGGCTA	TACAATGTGG	ATCAGGATCA	ACCATTCTTT	AGGTTCACTT	1560
GA CTC GCC AC	CAACGTGTGT	CCTTCCTGAC	TCCGTAGTAA	AACC ACT ACC	TCCATCTAAC	1620
GTAAAAGCAG	AGATTACTGT	AAACACTGGA	TTATTGAAAG	TATCTGGGA	AAAGCCAGTC	1680
TTTCCGGAGA	ATAACCTTCA	ATTCCAGATT	CGATATGGCT	TAAGTGGAAA	AGAAAATACAA	1740
TGGAAGACAC	ATGAGGTATT	CGATGCAAAG	TCAAAGTCTG	CCAGCCTGCT	GGTGTCA GAC	1800
CTCTGTGCAG	TCTATGTGGT	CCAGGTTCGC	TGCCGGCGGT	TGGATGGACT	AGGATATTGG	1860
AGTAATTGGA	GCAGTCCAGC	CTATACGCTT	GTCATGGATG	TA AAAGTTCC	TATGAGAGGG	1920
CCTGAATT TT	GGAGAAAAAT	GGATGGGGAC	GTTACTAAAA	AGGAGAGAAA	TGTCACCTTG	1980
CTTTGGAAGC	CCCTGACGAA	AAATGACTCA	CTGTGTAGTG	TGAGGAGGTA	CGTGGTGAAG	2040
CATCGTACTG	CCCACAATGG	GACGTGGTCA	GAAGATGTGG	GAAATCGGAC	CAATCTCACT	2100
TTCCTGTGGA	CAGAAC CAGC	GCACACTGTT	ACAGTTCTGG	CTGTCAATT C	CCTCGGCGCT	2160
TCCCTTGTGA	ATTTAACCT	TACCTTCTCA	TGGCCCATGA	GTAAAGTGAG	TGCTGTGGAG	2220
TCACTCAGTG	CTTATCCCCT	GAGCAGCAGC	TGTGT CATCC	TTTCCTGGAC	ACTGTCACCT	2280
GATGATTATA	GTCTGTTATA	TCTGGTTATT	GAATGGAAGA	TCCTTAATGA	AGATGATGGA	2340
ATGAAGTGGC	TTAGAATTCC	CTCGAATGTT	AAAAAGTTT	ATATCCACGA	TAATTTATT	2400
CCCATCGAGA	AATATCAGTT	TAGTCTTAC	CCAGTATT TA	TGGAAGGAGT	TGGAAAACCA	2460
AAGATAATT A	ATGGTTTCAC	CAAAGATGCT	ATCGACAAGC	AGCAGAATGA	CGCAGGGCTG	2520
TATGTCATTG	TACCCATAAT	TATTCCTCT	TGTGT CCTAC	TGCTCGGAAC	ACTGTTAATT	2580
TCACACCAGA	GAATGAAAAA	GTTGTTTGG	GACGATGTT C	CAAACCCCAA	GAATTGTTCC	2640
TGGGCACAAG	GA CTGAATT T	CCAAAAGGAT	ATATCTTAC	ATGAAGTTT	TATTTTCAGA	2700
TAG						2703

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 900 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Met	Cys	Gln	Lys	Phe	Tyr	Val	Val	Leu	Leu	His	Trp	Glu	Phe	Leu
1				5					10				15		
Tyr	Val	Ile	Ala	Ala	Leu	Asn	Leu	Ala	Tyr	Pro	Ile	Ser	Pro	Trp	Lys
	20				25				30						
Phe	Lys	Leu	Phe	Cys	Gly	Pro	Pro	Asn	Thr	Thr	Asp	Asp	Ser	Phe	Leu
	35				40			45							
Ser	Pro	Ala	Gly	Ala	Pro	Asn	Asn	Ala	Ser	Ala	Leu	Lys	Gly	Ala	Ser
	50				55			60							
Glu	Ala	Ile	Val	Glu	Ala	Lys	Phe	Asn	Ser	Ser	Gly	Ile	Tyr	Val	Pro
	65			70		75			80						
Glu	Leu	Ser	Lys	Thr	Val	Phe	His	Cys	Cys	Phe	Gly	Asn	Glu	Gln	Gly
	85				90		95								
Gln	Asn	Cys	Ser	Ala	Leu	Thr	Asp	Asn	Thr	Glu	Gly	Lys	Thr	Leu	Ala
	100				105		110								
Ser	Val	Val	Lys	Ala	Ser	Val	Phe	Arg	Gln	Leu	Gly	Val	Asn	Trp	Asp
	115				120		125								
Ile	Glu	Cys	Trp	Met	Lys	Gly	Asp	Leu	Thr	Leu	Phe	Ile	Cys	His	Met
	130				135		140								
Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys	Val	His
	145			150		155			160						
Leu	Leu	Tyr	Asp	Leu	Pro	Glu	Val	Ile	Asp	Asp	Ser	Pro	Leu	Pro	Pro
	165				170		175								
Leu	Lys	Asp	Ser	Phe	Gln	Thr	Val	Gln	Cys	Asn	Cys	Ser	Leu	Arg	Gly
	180				185		190								
Cys	Glu	Cys	His	Val	Pro	Val	Pro	Arg	Ala	Lys	Leu	Asn	Tyr	Ala	Leu
	195				200		205								
Leu	Met	Tyr	Leu	Glu	Ile	Thr	Ser	Ala	Gly	Val	Ser	Phe	Gln	Ser	Pro
	210			215		220									
Leu	Met	Ser	Leu	Gln	Pro	Met	Leu	Val	Val	Lys	Pro	Asp	Pro	Pro	Leu
	225			230		235		240							
Gly	Leu	His	Met	Glu	Val	Thr	Asp	Asp	Gly	Asn	Leu	Lys	Ile	Ser	Trp
	245			250		255									
Asp	Ser	Gln	Thr	Met	Ala	Pro	Phe	Pro	Leu	Gln	Tyr	Gln	Val	Lys	Tyr
	260			265		270									
Leu	Glu	Asn	Ser	Thr	Ile	Val	Arg	Glu	Ala	Ala	Glu	Ile	Val	Ser	Ala
	275			280		285									
Thr	Ser	Leu	Leu	Val	Asp	Ser	Val	Leu	Pro	Gly	Ser	Ser	Tyr	Glu	Val
	290			295		300									
Gln	Val	Arg	Ser	Lys	Arg	Leu	Asp	Gly	Ser	Gly	Val	Trp	Ser	Asp	Trp

305	310	315	320
Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro			
325	330	335	
Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr			
340	345	350	
Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg			
355	360	365	
Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp			
370	375	380	
Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg			
385	390	395	400
Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys			
405	410	415	
His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile			
420	425	430	
Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser			
435	440	445	
Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr			
450	455	460	
His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr			
465	470	475	480
Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys			
485	490	495	
Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg			
500	505	510	
Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu			
515	520	525	
Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu			
530	535	540	
Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val			
545	550	555	560
Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly			
565	570	575	
Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys			
580	585	590	
Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln			
595	600	605	
Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser			
610	615	620	
Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly			
625	630	635	640
Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg			
645	650	655	

Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
 660 665 670
 Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
 675 680 685
 Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
 690 695 700
 Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
 705 710 715 720
 Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
 725 730 735
 Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
 740 745 750
 Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
 755 760 765
 Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
 770 775 780
 Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Asp Asn Phe Ile
 785 790 795 800
 Pro Ile Glu Lys Tyr Gln Phe Ser Leu Tyr Pro Val Phe Met Glu Gly
 805 810 815
 Val Gly Lys Pro Lys Ile Ile Asn Gly Phe Thr Lys Asp Ala Ile Asp
 820 825 830
 Lys Gln Gln Asn Asp Ala Gly Leu Tyr Val Ile Val Pro Ile Ile Ile
 835 840 845
 Ser Ser Cys Val Leu Leu Leu Gly Thr Leu Leu Ile Ser His Gln Arg
 850 855 860
 Met Lys Lys Leu Phe Trp Asp Asp Val Pro Asn Pro Lys Asn Cys Ser
 865 870 875 880
 Trp Ala Gln Gly Leu Asn Phe Gln Lys Asp Ile Ser Leu His Glu Val
 885 890 895
 Phe Ile Phe Arg
 900

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: A20 (OB-Re)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGGAATCGT	TCTGCAAATC	CAGGTGTACA	CCTCTGAAGA	AAGATGATGT	GTCAGAAATT	60
CTATGTGGTT	TTGTTACACT	GGGAATTCT	TTATGTGATA	GCTGCACTTA	ACCTGGCATA	120
TCCAATCTCT	CCCTGGAAAT	TTAAGTTGTT	TTGTGGACCA	CCGAACACAA	CCGATGACTC	180
CTTTCTCTCA	CCTGCTGGAG	CCCCAAACAA	TGCCTCGGCT	TTGAAGGGGG	CTTCTGAAGC	240
AATTGTTGAA	GCTAAATTAA	ATTCAAGTGG	TATCTACGTT	CCTGAGTTAT	CCAAAACAGT	300
CTTCCACTGT	TGCTTGGGA	ATGAGCAAGG	TCAAAACTGC	TCTGCACTCA	CAGACAAACAC	360
TGAAGGGAAG	ACACTGGCTT	CAGTAGTGAA	GGCTTCAGTT	TTTCGCCAGC	TAGGTGTAAA	420
CTGGGACATA	GAGTGCTGGA	TGAAAGGGGA	CTTGACATTA	TTCATCTGTC	ATATGGAGCC	480
ATTACCTAAG	AACCCCTTCA	AGAATTATGA	CTCTAAGGTC	CATCTTTAT	ATGATCTGCC	540
TGAAGTCATA	GATGATTCGC	CTCTGCCCCC	ACTGAAAGAC	AGCTTTCAGA	CTGTCCAATG	600
CAACTGCAGT	CTTCGGGGAT	GTGAATGTCA	TGTGCCGGTA	CCCAGAGCCA	AACTCAACTA	660
CGCTCTTCTG	ATGTATTTGG	AAATCACATC	TGCCGGTGTG	AGTTTCAGT	CACCTCTGAT	720
GTCACTGCAG	CCCATGCTTG	TTGTGAAACC	CGATCCACCC	TTAGGTTGC	ATATGGAAGT	780
CACAGATGAT	GGTAATTAA	AGATTCTTG	GGACAGCCAA	ACAATGGCAC	CATTTCCGCT	840
TCAATATCAG	GTGAAATATT	TAGAGAATTC	TACAATTGTA	AGAGAGGCTG	CTGAAATTGT	900
CTCAGCTACA	TCTCTGCTGG	TAGACAGTGT	GCTTCCTGGA	TCTTCATATG	AGGTCCAGGT	960
GAGGAGCAAG	AGACTGGATG	GTTCAGGAGT	CTGGAGTGAC	TGGAGTTCAC	CTCAAGTCTT	1020
TACCACACAA	GATGTTGTGT	ATTTTCCACC	CAAATTCTG	ACTAGTGTG	GATCGAATGC	1080
TTCTTTCAT	TGCATCTACA	AAAACGAAAA	CCAGATTATC	TCCTCAAAAC	AGATAGTTG	1140
GTGGAGGAAT	CTAGCTGAGA	AAATCCCTGA	GATACAGTAC	AGCATTGTGA	GTGACCGAGT	1200
TAGCAAAGTT	ACCTTCTCCA	ACCTGAAAGC	CACCAAGACCT	CGAGGGAAGT	TTACCTATGA	1260
CGCAGTGTAC	TGCTGCAATG	AGCAGGCGTG	CCATCACCGC	TATGCTGAAT	TATACGTGAT	1320
CGATGTCAAT	ATCAATATAT	CATGTGAAAC	TGACGGGTAC	TTAACTAAAA	TGACTTGCAG	1380
ATGGTCACCC	AGCACAATCC	AATCACTAGT	GGGAAGCACT	GTGCAGCTGA	GGTATCACAG	1440
GCGCAGCCTG	TATTGTCCTG	ATAGTCCATC	TATTCACTCCT	ACGTCTGAGC	CCAAAAACTG	1500
CGTCTTACAG	AGAGACGGCT	TTTATGAATG	TGTTTCCAG	CCAATCTTC	TATTATCTGG	1560
CTATACAATG	TGGATCAGGA	TCAACCATTG	TTTAGGTTCA	CTTGACTCGC	CACCAACGTG	1620
TGTCCTTCCT	GAECTCGTAG	TAAAACCACT	ACCTCCATCT	AACGTAAAAG	CAGAGATTAC	1680
TGTAAACACT	GGATTATTGA	AAGTATCTTG	GGAAAAGCCA	GTCTTCCGG	AGAATAACCT	1740
TCAATTCCAG	ATTCGATATG	GCTTAAGTGG	AAAAGAAATA	CAATGGAAGA	CACATGAGGT	1800
ATTCGATGCA	AAGTCAAAGT	CTGCCAGCCT	GCTGGTGTCA	GACCTCTGTG	CAGTCTATGT	1860

GGTCCAGGTT CGCTGCCGGC GGTTGGATGG ACTAGGATAT TGGAGTAATT GGAGCAGTCC	1920
AGCCTATAACG CTTGTCAATGG ATGTAAAAGT TCCTATGAGA GGGCCTGAAT TTTGGAGAAA	1980
AATGGATGGG GACGTTACTA AAAAGGAGAG AAATGTCACC TTGCTTGGA AGCCCCTGAC	2040
GAAAAATGAC TCACTGTGTA GTGTGAGGAG GTACGTGGTG AAGCATCGTA CTGCCACAA	2100
TGGGACGTGG TCAGAAGATG TGGGAAATCG GACCAATCTC ACTTTCTGT GGACAGAAC	2160
AGCGCACACT GTTACAGTTC TGGCTGTCAA TTCCCTCGGC GCTTCCCTTG TGAATTTAA	2220
CCTTACCTTC TCATGGCCA TGAGTAAAGT GAGTGCTGTG GAGTCACTCA GTGCTTATCC	2280
CCTGAGCAGC AGCTGTGTCA TCCTTCCTG GACACTGTCA CCTGATGATT ATAGTCTGTT	2340
ATATCTGGTT ATTGAATGGA AGATCCTAA TGAAGATGAT GGAATGAAGT GGCTTAGAAT	2400
TCCCTCGAAT GTTAAAAAGT TTTATATCCA CGGTATGTGT ACTGTACTTT TCATGGATTA	2460
G	2461

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 805 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Cys Gln Lys Phe Tyr Val Val Leu Leu His Trp Glu Phe Leu			
1	5	10	15
Tyr Val Ile Ala Ala Leu Asn Leu Ala Tyr Pro Ile Ser Pro Trp Lys			
20	25	30	
Phe Lys Leu Phe Cys Gly Pro Pro Asn Thr Thr Asp Asp Ser Phe Leu			
35	40	45	
Ser Pro Ala Gly Ala Pro Asn Asn Ala Ser Ala Leu Lys Gly Ala Ser			
50	55	60	
Glu Ala Ile Val Glu Ala Lys Phe Asn Ser Ser Gly Ile Tyr Val Pro			
65	70	75	80
Glu Leu Ser Lys Thr Val Phe His Cys Cys Phe Gly Asn Glu Gln Gly			
85	90	95	
Gln Asn Cys Ser Ala Leu Thr Asp Asn Thr Glu Gly Lys Thr Leu Ala			
100	105	110	

Ser Val Val Lys Ala Ser Val Phe Arg Gln Leu Gly Val Asn Trp Asp
 115 120 125
 Ile Glu Cys Trp Met Lys Gly Asp Leu Thr Leu Phe Ile Cys His Met
 130 135 140
 Glu Pro Leu Pro Lys Asn Pro Phe Lys Asn Tyr Asp Ser Lys Val His
 145 150 155 160
 Leu Leu Tyr Asp Leu Pro Glu Val Ile Asp Asp Ser Pro Leu Pro Pro
 165 170 175
 Leu Lys Asp Ser Phe Gln Thr Val Gln Cys Asn Cys Ser Leu Arg Gly
 180 185 190
 Cys Glu Cys His Val Pro Val Pro Arg Ala Lys Leu Asn Tyr Ala Leu
 195 200 205
 Leu Met Tyr Leu Glu Ile Thr Ser Ala Gly Val Ser Phe Gln Ser Pro
 210 215 220
 Leu Met Ser Leu Gln Pro Met Leu Val Val Lys Pro Asp Pro Pro Leu
 225 230 235 240
 Gly Leu His Met Glu Val Thr Asp Asp Gly Asn Leu Lys Ile Ser Trp
 245 250 255
 Asp Ser Gln Thr Met Ala Pro Phe Pro Leu Gln Tyr Gln Val Lys Tyr
 260 265 270
 Leu Glu Asn Ser Thr Ile Val Arg Glu Ala Ala Glu Ile Val Ser Ala
 275 280 285
 Thr Ser Leu Leu Val Asp Ser Val Leu Pro Gly Ser Ser Tyr Glu Val
 290 295 300
 Gln Val Arg Ser Lys Arg Leu Asp Gly Ser Gly Val Trp Ser Asp Trp
 305 310 315 320
 Ser Ser Pro Gln Val Phe Thr Thr Gln Asp Val Val Tyr Phe Pro Pro
 325 330 335
 Lys Ile Leu Thr Ser Val Gly Ser Asn Ala Ser Phe His Cys Ile Tyr
 340 345 350
 Lys Asn Glu Asn Gln Ile Ile Ser Ser Lys Gln Ile Val Trp Trp Arg
 355 360 365
 Asn Leu Ala Glu Lys Ile Pro Glu Ile Gln Tyr Ser Ile Val Ser Asp
 370 375 380
 Arg Val Ser Lys Val Thr Phe Ser Asn Leu Lys Ala Thr Arg Pro Arg
 385 390 395 400
 Gly Lys Phe Thr Tyr Asp Ala Val Tyr Cys Cys Asn Glu Gln Ala Cys
 405 410 415
 His His Arg Tyr Ala Glu Leu Tyr Val Ile Asp Val Asn Ile Asn Ile
 420 425 430
 Ser Cys Glu Thr Asp Gly Tyr Leu Thr Lys Met Thr Cys Arg Trp Ser
 435 440 445
 Pro Ser Thr Ile Gln Ser Leu Val Gly Ser Thr Val Gln Leu Arg Tyr
 450 455 460

His Arg Arg Ser Leu Tyr Cys Pro Asp Ser Pro Ser Ile His Pro Thr
 465 470 475 480
 Ser Glu Pro Lys Asn Cys Val Leu Gln Arg Asp Gly Phe Tyr Glu Cys
 485 490 495
 Val Phe Gln Pro Ile Phe Leu Leu Ser Gly Tyr Thr Met Trp Ile Arg
 500 505 510
 Ile Asn His Ser Leu Gly Ser Leu Asp Ser Pro Pro Thr Cys Val Leu
 515 520 525
 Pro Asp Ser Val Val Lys Pro Leu Pro Pro Ser Asn Val Lys Ala Glu
 530 535 540
 Ile Thr Val Asn Thr Gly Leu Leu Lys Val Ser Trp Glu Lys Pro Val
 545 550 555 560
 Phe Pro Glu Asn Asn Leu Gln Phe Gln Ile Arg Tyr Gly Leu Ser Gly
 565 570 575
 Lys Glu Ile Gln Trp Lys Thr His Glu Val Phe Asp Ala Lys Ser Lys
 580 585 590
 Ser Ala Ser Leu Leu Val Ser Asp Leu Cys Ala Val Tyr Val Val Gln
 595 600 605
 Val Arg Cys Arg Arg Leu Asp Gly Leu Gly Tyr Trp Ser Asn Trp Ser
 610 615 620
 Ser Pro Ala Tyr Thr Leu Val Met Asp Val Lys Val Pro Met Arg Gly
 625 630 635 640
 Pro Glu Phe Trp Arg Lys Met Asp Gly Asp Val Thr Lys Lys Glu Arg
 645 650 655
 Asn Val Thr Leu Leu Trp Lys Pro Leu Thr Lys Asn Asp Ser Leu Cys
 660 665 670
 Ser Val Arg Arg Tyr Val Val Lys His Arg Thr Ala His Asn Gly Thr
 675 680 685
 Trp Ser Glu Asp Val Gly Asn Arg Thr Asn Leu Thr Phe Leu Trp Thr
 690 695 700
 Glu Pro Ala His Thr Val Thr Val Leu Ala Val Asn Ser Leu Gly Ala
 705 710 715 720
 Ser Leu Val Asn Phe Asn Leu Thr Phe Ser Trp Pro Met Ser Lys Val
 725 730 735
 Ser Ala Val Glu Ser Leu Ser Ala Tyr Pro Leu Ser Ser Ser Cys Val
 740 745 750
 Ile Leu Ser Trp Thr Leu Ser Pro Asp Asp Tyr Ser Leu Leu Tyr Leu
 755 760 765
 Val Ile Glu Trp Lys Ile Leu Asn Glu Asp Asp Gly Met Lys Trp Leu
 770 775 780
 Arg Ile Pro Ser Asn Val Lys Lys Phe Tyr Ile His Gly Met Cys Thr
 785 790 795 800
 Val Leu Phe Met Asp
 805

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Ra

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn	Phe	Gln	Lys	Arg	Thr	Asp	Leu
1							5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rb

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asn	Phe	Gln	Lys	Pro	Glu	Thr	Phe	Glu	Gln	Leu	Phe	Thr	Lys	His	Ala
1					5				10				15		
Glu	Ser	Val	Ile	Phe	Gly	Pro	Leu	Leu	Leu	Glu	Pro	Glu	Pro	Ile	Ser
								20	25			30			
Glu	Glu	Ile	Ser	Val	Asp	Thr	Ala	Trp	Lys	Asn	Lys	Asp	Glu	Met	Val
					35			40			45				
Pro	Ala	Ala	Met	Val	Ser	Leu	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Glu	Ser
				50			55			60					
Ser	Ser	Ile	Cys	Ile	Ser	Asp	Gln	Cys	Asn	Ser	Ala	Asn	Phe	Ser	Gly
					65		70			75			80		

Ser Gln Ser Thr Gln Val Cys Glu Asp Glu Cys Gln Arg Gln Pro Ser
 85 90 95
 Val Lys Tyr Ala Thr Leu Val Ser Asn Asp Lys Leu Val Glu Thr Asp
 100 105 110
 Glu Glu Gln Gly Phe Ile His Ser Pro Val Ser Asn Cys Ile Ser Ser
 115 120 125
 Asn His Ser Pro Leu Arg Gln Ser Phe Ser Ser Ser Trp Glu Thr
 130 135 140
 Glu Ala Gln Thr Phe Phe Leu Leu Ser Asp Gln Gln Pro Thr Met Ile
 145 150 155 160
 Ser Pro Gln Leu Ser Phe Ser Gly Leu Asp Glu Leu Leu Glu Leu Glu
 165 170 175
 Gly Ser Phe Pro Glu Glu Asn His Arg Glu Lys Ser Val Cys Tyr Leu
 180 185 190
 Gly Val Thr Ser Val Asn Arg Arg Glu Ser Gly Val Leu Leu Thr Gly
 195 200 205
 Glu Ala Gly Ile Leu Cys Thr Phe Pro Ala Gln Cys Leu Phe Ser Asp
 210 215 220
 Ile Arg Ile Leu Gln Glu Arg Cys Ser His Phe Val Glu Asn Asn Leu
 225 230 235 240
 Ser Leu Gly Thr Ser Gly Glu Asn Phe Gly Pro Tyr Met Pro Gln Phe
 245 250 255
 Gln Thr Cys Ser Thr His Ser His Lys Ile Met Glu Asn Lys Met Cys
 260 265 270
 Asp Phe Thr Val
 275

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rc
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asn Phe Gln Lys Val Thr Val
 1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Rd

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Phe Gln Lys Asp Ile Ser His Glu Val Phe Ile Phe Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: C-terminal
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: OB-Re

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Tyr Ile His Gly Met Cys Thr Val Leu Phe Met Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Ra/db/db

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Pro Gln Lys Arg Thr Asp Thr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: OB-Rb/wt

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Gln Lys Pro Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGGAGGGA AA

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GATGGAGGTA AA

12

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCTTGGGTT CTCTGAAGAA

20

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATTGTCA GTCACAGCCT C

21

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCTGAATTG GAATCAAATA CAC

23

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAATCTGTTA TCCTTCTGAA AC

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACACTGTTAA TTTCACACCA GAG

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGTCATTCAA ACCATTAGTT TAGG

24

- (2) INFORMATION FOR SEQ ID NO:26:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGGATAAACCC CTTGCTCTTC A

21

- (2) INFORMATION FOR SEQ ID NO:27:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGAACACAAAC AACATAAAGC CC

22

- (2) INFORMATION FOR SEQ ID NO:28:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGCTCCCTC AGGGCCAC

18

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGACTGAAT GAAGATGTAA TATAC

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGTTATATCT GGTTATTGAA TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATTAATGA TTTATTATCA GAATTGC

27

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu	Pro	Leu	Pro	Lys	Asn	Pro	Phe	Lys	Asn	Tyr	Asp	Ser	Lys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

His	Arg	Arg	Ser	Leu	Tyr	Cys	Pro	Asp	Ser	Pro	Ser	Ile	His	Pro	Thr
1				5					10				15		

Ser	Glu	Pro	Lys
		20	

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: not relevant

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln	Arg	Met	Lys	Lys	Leu	Phe	Trp	Asp	Asp	Val	Pro	Asn	Pro	Lys	Asn
1					5					10				15	
Cys Ser Trp															

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGGNAAGCG	CCGAGGGAAT	TGACAGCCAG	AACTGTAACA	GTGTGCGCTG	GTTCTGTCCA	60
CAGGAAAGTG	AGATTGGTCC	GATTTCCCAC	ATCTTCTGAC	CACGTCCCAT	TGTGGGCAGT	120
ACGATGCTTC	ACCACGTACC	TCCTCACACT	ACACAGTGAG	TCATTT		166

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTGAAGCAT CGTACTGCCA	ACAATGGGAC GTGGTCAGAA	GATGTGGAA ATCGGACCAA	60
TCTCACTTTC CTGTGGACAG	AACCAGCGCA CACTGTTACA	GTTCTGGCTG TCAATTCCCT	120
CGGCGCTTCC CTTGTGAATT	TTAACCTTAC CTTCTCATGG	CCCATGAGTA AAGTGAGTGC	180
TGTGGAGTCA CTCAGTGCTT	ATCCCCTGAG CAGCAGCTGT	GTCATCCTTT CCTGGACACT	240
GTCACCTGAT GATTATAGTC	TGTTATATCT GGTTATTGAA	TGGAAGATCC TTAATGAAGA	300
TGATGGAATG AAGTGGCTTA			320

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 42

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GATTACTGGA GATGCAGTTG	GTGACAGGAC TATGGATAAA	CCCTTGCTCT TCATCAGTTT	60
CCACTAGTTT ATCGTTGCTG	ACCAAGAGTTG CATATTAAAC	TGAGGGTTGT CTCTGACACT	120
CATCCTCACCA GGTTACCTGG	GTGCTCTGAG ACCCAGAG		158

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGAGAGATCC CTGACCCTAG TTAGATCTGT TTTCAAGGCTC TGTGTTCAT	TGATGTTCAG	60
AAGTCAGCAA GGTTCTCATA TGTCTGAGT TAGTAAGATG TCTCAGGGTT CCCCCATCAG		120
CTAACAAACCA CTTTGACATG AGAAGGCAGA AAGTTAAAGA ACACACTACTG GTGTTTTACT		180
TAAAGATACG AG		192

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGACTGACAA GGAAGTTTC TCATCTAACAGCAAGCAAA GGAACTGCTT ATGTNCTGTG	60
ANGAACCAAG GNAGCTCAGA TGTCACCATA GTCATCATGA ACTCGAGTGA CTCTGCCACT	120
GTTCCCCCAG GATGTGCTTG GANGATAATC CTGCGCAAGA AACAGATA	
168	

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: S3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAATTATGA CTCTAAGGTC CATGTTTAT ATGATCTGCC TGAAGTCATA GATGATT CGC	60
---	----

CTCTGCCCCC ACTGAAAGAC AGNTTCAGA CTGTCCAATG NAACTGCAGT CTTCGGGGAT	120
GTGAATGTCA TGTGCCAGTA CCCAGAGCCA AACTCAACTA CGCTCTCTG ATGTATTGG	180
NAATCACATC TGCCGGTGTG AGTTTCAGT CACCTCTGAT GTCACTGCAG CCCATGCTTG	240
TTGTGAAACC CGATCCACC	259

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTCAACAAT TGGTCAGAA GCCCCCTTCA AAGCCGAGGC ATTGTTGGG GCTCCAGCAG	60
GTGAGAGAAA GGAGTCATCG GTTGTGTTCG GTGGTCCACA AAACAACTTA AATTTCCAGG	120
GAGAGATTGG ATATGCCAGG TTAAGTGCAG CTATCACATA AAGAAATTCC CAGTGTAACA	180
AAACCACATA GANTTTCTAA CACATCATCT TTCTTCAGAG GTGTACACCT GGATTTGCAG	240
AACGATTCCCT	250

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGAGGGAAT TGACAGCC	18
---------------------	----

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCACTGTGT AGTGTGAGGA GG

22

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCTGTGGAC AGAACCCAGC

19

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TGACACAGCT GCTGCTCAG

19

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCTCAGAG CACCCAGGTA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGAGAGATCC CTGACCCTAG TT

22

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AACTTTCTGC CTTCCCTCTC ATGTCA

26

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTCTCATCT AACAAAGCAAG CA

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATCTGTTTCT TGCGCAGGAT

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CATTGTTTGG GGCTCCAG

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATCGTTCTG CAAATCCAGG

20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGAAGTCATA GATGATT CGC C

21

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTCGTACCC GACGTCACTG

20